

Claims

1. A method for transforming a useful plant by introducing a gene of another species into the useful plant wherein the region of a factor relating to the poly (A) addition of the mRNA of the useful plant to be transformed contained in the base sequence of the gene of the other species is modified into another base sequence not relating to the poly (A) addition of the mRNA without substantially altering the function of the protein encoded by the gene to be introduced.
2. The method according to claim 1, wherein the gene of another species to be introduced is derived from yeast.
3. The method according to claim 1 or 2, wherein the region of a factor relating to the poly (A) addition of the mRNA is a base sequence having AATAAA like sequence.
4. The method according to claim 3, wherein the region of a factor relating to the poly (A) addition of the mRNA is located in a downstream from the GT-rich base sequence.
5. The method according to any one of claims 1-4, wherein the modification of base sequence in the region of a factor relating to the poly (A) addition of the mRNA is performed based on a codon usage of the useful higher plant to be transformed.
6. The method according to any one of claims 1-5, wherein the modification of base sequence is performed so that the region rich in base G and base T is reduced.
7. The method according to any one of claims 1-6, wherein the modification of base sequence comprises small difference between base G and base C covering throughout the region of gene to be introduced.
8. The method according to any one of claims 1-7, wherein the modification of base sequence is performed so as not to have ATTTA sequence.

9. The method according to any one of claims 1-8, characterized by having Kozak sequence in the upstream of the initiation codon of the gene to be introduced.
10. The method according to any one of claims 1-9, wherein the gene to be introduced encodes a protein involved in absorption of nutrition.
11. The method according to claim 10, wherein the gene to be introduced is the gene encoding ferric-chelate reductase FRE1.
12. The method according to claim 11, wherein the gene encoding ferric-chelate reductase FRE1 is derived from yeast.
13. The method according to any one of claims 1-12, wherein the useful plant is grass.
14. The method according to any one of claims 1-12, wherein the useful plant is tobacco.
15. A transformed useful plant which can be produced by the method according to claims 1-14.
16. The plant according to claim 15, wherein the plant is seed.
17. A nucleic acid having modified base sequence which can be used by the method according to any one of claims 1-14.
18. The nucleic acid according to claim 17, wherein the nucleic acid is DNA.
19. The DNA according to claim 18, wherein the gene to be introduced is the DNA encoding ferric-chelate reductase FRE1.
20. The DNA according to claim 19, wherein the DNA has a base sequence of SEQ ID NO:1.
21. A method for producing the nucleic acid according to any one of claims 17-20, wherein the nucleic acid is cleaved into several fragments and these fragments are ligated.